

<110> Nara Institute of Science, Technology, Research Institute of Innovative Technology  
for the Earth and Kinki University

<130> C01F1576

<210> 1

&lt;212&gt; PRT

## <220> Fructose-1,6-bisphosphatase

<400> 1

Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met  
20 25 30

Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser  
50 55 60

Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg  
85 90 95

Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp  
115 120 125

Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp  
145 150 155 160

Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met  
180 185 190

Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr

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195	200	205
Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu		
210	225	220
Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly		
225	230	235
Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu		
245	250	255
Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly		
260	265	270
Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr		
275	280	285
Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu		
290	295	300
Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys		
305	310	315
Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile		
325	330	335
His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys		
340	345	350
Leu Glu Lys Tyr Leu Ala		

355

&lt;210&gt; 2

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Fructose-1,6-bisphosphatase

&lt;223&gt;

&lt;400&gt; 2

gcagccgtag gagaggcggc tacagaaaca aaggcaagga ctagaagtaa gtacgaaatt	60
gaaacactaa caggctggct gcttaaaca gaaatggcag gtgttatiga tgcigaactt	120
accatcgctt tttctagcat ttcatggct tgtaaacaaa ttgcttccit ggttcaacga	180
gctggatatt ctaacttgac tggaaatcaa ggtgcigtca atatccaagg agaggatcag	240
aagaaacttg atgttgtct caatgaggtg ttttcgagct gcttgagatc gattggaaga	300
acaggaataa tagcatcaga agaagaggat gtaccagtgg cagtggaaga gattactct	360
ggaaactata ttgttgtgt tgaaccacti gatgggtcat ccaacattga tgcagctgtc	420
tccactgggt ccatctttgg catttatagc cctaacgatg agtgcattgt tgactctgat	480
cacgacgatg agtcacagct aagtcagaa gaacagaggt gtgtagttaa tgtatgtcaa	540
ccaggggata acctattagc agcagggtat tgtatgtact caagctctgt tatcttcgta	600
citacaattg gtaaagggtg gtaatgattc acattagatc caatgtatgg tgaattcgta	660
cicacitcag agaaaatcca aatcccaaaa gctgggaaga tctattcatt caatgaaggt	720

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aactacaaaa tgtgggatga taaattgaag aaglacatgg atgatcttaa agagccagga 780  
 gattcacaga aaccgtactc gctcgttac ataggagatt tagttgggga ctltcataga 840  
 acacttttat atggtgggat ttaiggttac ccaagagatg caaagagtaa gaatgggaaa 900  
 ttgaggcttt tglatgaatg tgcacctatg agttttatig ttgaacaagc tggtagttaa 960  
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 ccactgtaca tcgggagigt ggaggaagta gagaaattag agaagtactt agca 1074

&lt;210&gt; 3

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Sedoheptulose-1,7-bisphosphatase

&lt;223&gt;

&lt;400&gt; 3

Val Asn Lys Ala Lys Asn Ser Ser Leu Val Thr Lys Cys Glu Leu Gly  
                   5                  10                  15  
 Asp Ser Leu Glu Glu Phe Leu Ala Lys Ala Thr Thr Asp Lys Gly Leu  
                   20                  25                  30  
 Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe  
                   35                  40                  45  
 Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe  
                   50                  55                  60  
 Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe  
 65                  70                  75                  80  
 Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu  
                   85                  90                  95  
 Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser  
                   100                  105                  110  
 Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe  
                   115                  120                  125  
 Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly  
                   130                  135                  140  
 Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro  
 145                  150                  155                  160  
 Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu  
                   165                  170                  175  
 Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr  
                   180                  185                  190  
 Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr  
                   195                  200                  205  
 Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu

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210	215	220
Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln		
225	230	235
Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr		240
	245	250
Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe		255
	260	265
Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val		270
	275	280
Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr		285
	290	295
Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser		300
305	310	315
Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala		320
	325	330

&lt;210&gt; 4

&lt;211&gt; 999

&lt;212&gt; DNA

<213> *Spinacia oleracea* L

&lt;220&gt; Sedoheptulose-1,7-bisphosphatase

&lt;223&gt;

&lt;400&gt; 4

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gaagcattaa ggaccattgg cttaaagtg aggactgctt catgtgggtg aactcaatgt	180
gttaacacct ttggagacga acagcttgcc atlgatgtgc ttgctgacaa gcttcttttc	240
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caagatatgg gaggccccgt tgatggcgga ttcagtgtag catttgacc ccttgatgga	360
tccagcattg tcgataccaa tttctcagtt gggaccatat tcgggggttg gccaggtgac	420
aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttaatggcct	480
aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttcttctt	540
gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc	600
tgtccigga acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac	660
tataataaag agaaatacac attgagatac actggaggaa tggttcctga tgttaaccag	720
atcatagtga aggagaaagg tataattcaca aatglaatat cacctacagc caaggcaaag	780
tigaggtiac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tgggtgtcac	840
agcagtgagg gaaccaagtc tgtgttggac attgaagtca aaaaccttga tgacagaacc	900
caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc	960
tctaggctag aggagccagt tctgtttgga gctgctgct	999

&lt;210&gt; 5

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&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Synechococcus

&lt;220&gt; fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus

PCC 7942

&lt;223&gt;

&lt;400&gt; 5

Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala  
5 10 15

Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala  
20 25 30

Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu  
35 40 45

Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro  
50 55 60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys  
65 70 75 80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val  
85 90 95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser  
100 105 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro  
115 120 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys  
130 135 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu  
145 150 155 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg  
165 170 175

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg  
180 185 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly  
195 200 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro  
210 215 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe  
225 230 235 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile  
245 250 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile

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260 265 270  
 Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln  
 275 280 285  
 Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu  
 290 295 300  
 Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile  
 305 310 315 320  
 Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe  
 325 330 335  
 Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp  
 340 345 350  
 Arg Pro Glu Arg  
 355

&lt;210&gt; 6

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Synechococcus

<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus  
 PCC. 7942

&lt;400&gt; 6

atcgcaacta aagccagaga tgtgaggagg ggatccggcc ttigttagac tcaactgttg 60  
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 cgaaaagaat gaagccgac gcgtcgcagt agaagcgatg cgggtgcgga tgaaccaagt 240  
 ggaaatgctg ggccgcatcg tcatcggtga aggcgagcgc gacgaagcac cgaigctcta 300  
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tccigatccc aaatggcggc cggagcggta gaacgggtat agctcgatcg cticggicgt	1200
tgtttttcag cgaatccatt tgcgacgct tttcaaacc llltttcgtc aaccttctll	1260
aaacggccic atgcatctcg cagttgtcgg cticagccatc ggacagcacc gg	1312

&lt;210&gt; 7

&lt;211&gt; 133

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA promoter

&lt;400&gt; 7

agcttctaca tacaccttgg ttgacacgag tatataagtc atgttatact gttgaataac	60
aagccctcca ttttctatit tgattttagt aaaactagt tgcttgggag tccctgatga	120
ttaaataaac caa	133

&lt;210&gt; 8

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rps16 terminator

&lt;400&gt; 8

agcttgaaat tcaattaagg aaataaatta aggaaataca aaaagggggg tagtcatttg	60
tatataactt tgtatgactt ttctcttcta tttttttgta tttccctccct ttccttttct	120
atttgtatit ttttatcatt gcttccattg aattactag	159

&lt;210&gt; 9

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;223&gt; aadA

&lt;400&gt; 9

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gcgtcatcga gcgccatctc gaaccgacgt tgctggccgt acatttgtac ggctccgcag	120
tggatggcgg cctgaagcca cacagtata ttgatttgct gggtacggtg accgtaaggc	180
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cgtggcgcta tccagctaag cgcgaactgc aatttggaga atggcagcgc aatgacattc	360
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cccagiatca gcccgtaata ctlgaagcta gacaggctta tctlggacaa gaagaagatc	720

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gcttggcctc gcgcgcagat cagttggaag aatttgtcca ctacgtgaaa ggcgagatca 780  
 ctaaggtagt tggcaaataa ctgca 805

<210> 10

<211> 4591

<212> DNA

<213> Artificial sequence

<223> pLD6

<400> 10

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 ggaagagtat gagtattcaa catitccgtg tgcgccittat tccctttttt gcggcatitt 180  
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tataagtcac gttatactgt tgaataacaa gccctccatt ttctattttg attttagaa 3660  
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&lt;210&gt; 11

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; multi-cloning regions

&lt;400&gt; 11

ccaagatcta aaaggagaaa ttaagcatgc tctagatcga tgaattcgcc c 51

&lt;210&gt; 12

&lt;211&gt; 142

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rrn promoter

&lt;400&gt; 12

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 cttggataca gttgtaggga gg 142

&lt;210&gt; 13

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA terminator

&lt;400&gt; 13

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 cttgtttctc ttcttgctaa tgttactata tctttttgat ttttttttc caaaaaaaaa 300  
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 tatcatggaa ataagaaaga agagctatat 390

&lt;210&gt; 14

&lt;211&gt; 5581

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; pLD200

&lt;400&gt; 14

11/14

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 c 5581

&lt;210&gt; 15

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Nicotiana tabacum*

&lt;223&gt; rbcL

&lt;400&gt; 15

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&lt;210&gt; 16

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; accD

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; polylinker

&lt;400&gt; 17

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21

&lt;210&gt; 18

&lt;211&gt; 7

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; Shine-Dalgarno Sequence

&lt;400&gt; 18

aggaggu

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